











# [JM] Submission

Acknowledgement > External





Inbox



Amin Fatoni 31 Aug 2020 to me v



### Emmy Yuanita:

Thank you for submitting the manuscript, "Molecular Docking of Xanthone Derivatives as therapeutic agent for covid19" to Molekul. With the online journal management system that we are using, you will be able to track its progress through the editorial process by logging in to the journal web site:

### Manuscript URL:

https://ojs.jmolekul.com/ojs/i ndex.php/jm/author/submission/701

Username: emmy\_yuanita

If you have any questions, please contact me. Thank you for considering this journal as a venue for your work.

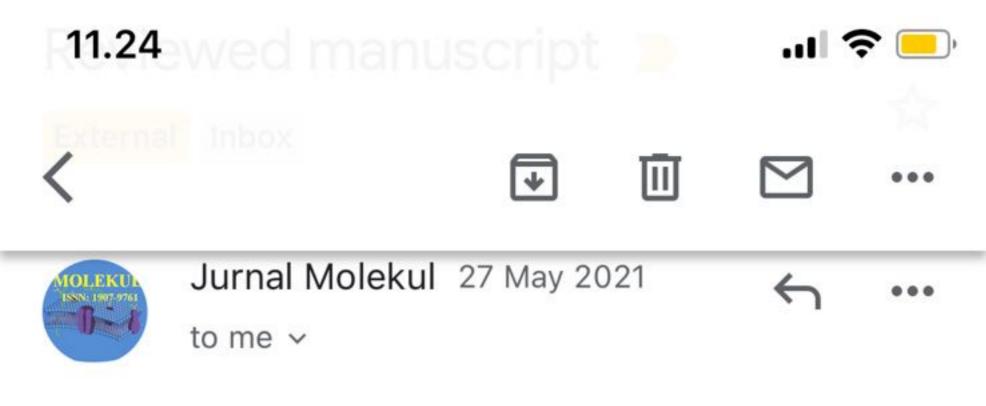












Dear authors,

We have reached a decision regarding your submission to Molekul, "Molecular Docking of Xanthone Derivatives as therapeutic agent for covid19".

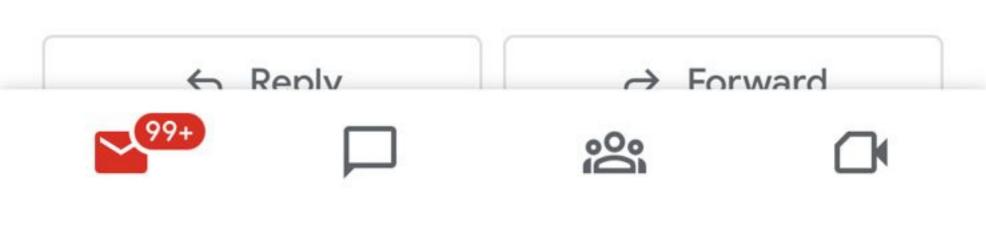
Our decision is: Revisions Required

Terlampir adalah hasil review reviewer#1. Mohon diperbaiki sesuai saran reviewer. Kami masih menunggu hasil review reviewer#2.

Terima kasih.

Ely Setiawan
Department of Chemistry, Faculty of
Mathematics and Natural Sciences,
Universitas Jenderal Soedirman, Purwokerto
elsant 13@yahoo.com

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# Reviewed manuscript >>



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Jurnal Molekul 27 May 2021 to me ~





Dear authors,

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## Reviewed manuscript >>



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Jurnal Molekul 9 Aug 2021 to me v







Dear authors,

We have reached a decision regarding your submission to Molekul, "Molecular Docking of Xanthone Derivatives as therapeutic agent for covid19", please revise according to the suggestion.

Our decision is: Revisions Required

- 1. Attached is a reviewed manuscript from reviewer#1.
- 2. Reviewer#2 comments:
  - The author should mention the type of protein used in this research in the abstract, i.e. protease, RdRp, etc.
  - Please make consistent writing of amino acid residues.
  - Make some corrections about what is covid-19 stands for, it should be "coronavirus disease 2019".
  - The authors did not mention what "CoV" stands for hafore using this term











 Please separate the docked conformation figures between the two targeted proteins. Do not combine in Figure 1.

"Binding Interactio → amir III acid

- The authors have not mentioned the redocking result, including the interacting residues, binding distance and binding energy between the proteins and native ligands. Please include this result as a comparison. Also, the docking result using therapeutic drugs such as remdesivir was strongly suggested.
- The authors should compare their results to the correlated recent studies which used similar methods.

Thank you.

Ely Setiawan

Department of Chemistry, Faculty of

Mathematics and Natural Sciences,

Universitas Jenderal Soedirman, Purwokerto

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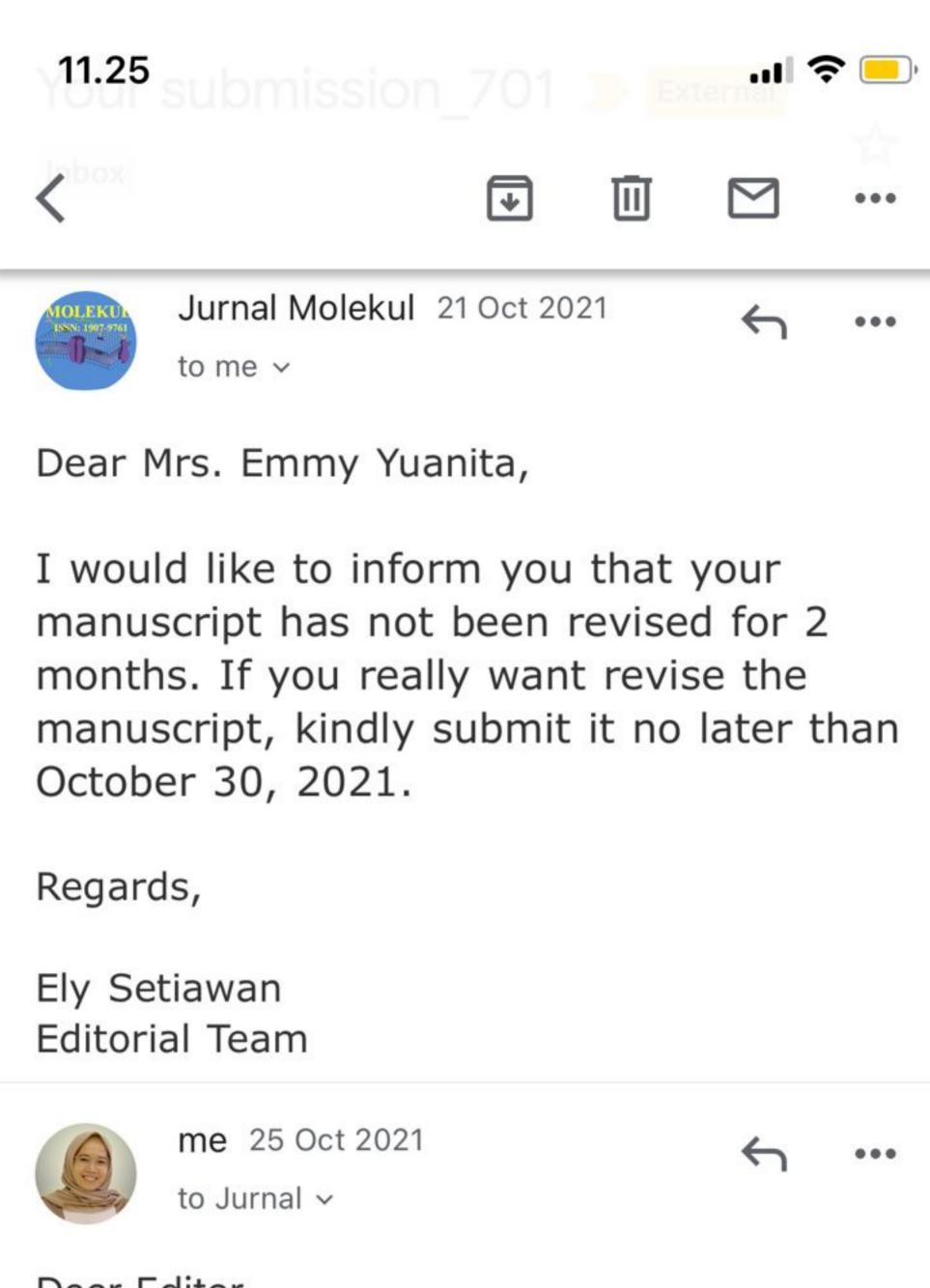
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Dear Editor
The following is a revision of the manuscript, sorry for the delay

sincerely

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## Proof Read - Jurnal MOLEKUL

Vol 17 No 1 > External Inbox







Jurnal Molekul 7 Mar 2022

to me v



### Yth. Dr. Emmy Yuanita, dkk

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> Terlampir file artikel yang telah di layout, mohon untuk dicek kembali (proofread). Untuk memastikan artikel anda terbit pada waktunya, mohon jika ada koreksi harap diperbaiki dan dikembalikan dalam waktu maksimal 2 hari. Adanya kesalahan setelah artikel diterbitkan atau dicetak tidak memungkinkan untuk direvisi lagi. Jika dalam batas waktu yang ditentukan tidak ada tanggapan, maka kami anggap penulis telah setuju dengan artikel tersebut baik isi, susunan penulis, dan komponen artikel lainnya.

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- Artikel akan diterbitkan diwebsite kami yan baru, mohon register dan submit difile terakhir ini di website kami yang baru: <a href="http://jos.unsoed.ac.id/index.php/jm/">http://jos.unsoed.ac.id/index.php/jm/</a>
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Yours sincerely,

MOLEKUL Editorial Team